

Input file T198sHVEM1; Output File T198sHVEM1.pat
Sequence length 1929

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CCACCCAGCAGGCCTGAGCCCCCTCTGTGCTGCCAGACACCCCCCTGTGCCCCACTCTCTGTGCTGCTCGGGTTCTGAGGCA 158
CAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTTCTGGCCCACAGCCGAGCAATGGCGCTGAGTT 237
CCTCTGTGCTGGAGTTCATCCTGTAGCTGGGTTCCCCGAGCTGCCGGTCTGAGCCTGAGGC M E P P G 5
ATG GAG CCT CCT GGA 311
D W G P P P W R S T P R T D V L R L V L 25
GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG 371
Y L T F L G A P C Y A P A L P S C K E D 45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC 431
E Y P V G S E C C P K C S P G Y R V K E 65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG 491
A C G E L T G T V C E P C P P G T Y I A 85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC 551
H L N G L S K C L Q C Q M C D P A M G L 105
GAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG 611
R A S R N C S R T E N A V C G C S P G H 125
GCG GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC 671
F C I V Q D G D H C A A C R A Y A T S S 145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC 731
P G Q R V Q K G G T E S Q D T L C Q N C 165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC 791
P P G T F S P N G T L E E C Q H Q T N R 185
GGC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA 851
A W K S Q T D L * 194
GCT TGG AAA AGT CAG ACA GAC CTC TGA 878
GGTCTCATCCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGG 957
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GTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCAAACCACTGACCCACAGACTCTGCACCCCGACGCC 1352
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GCCCTGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGTGTTGGGTAGAGCTGGGGACGCCACGTGC 1510
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CGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTG 1747
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Figure 1

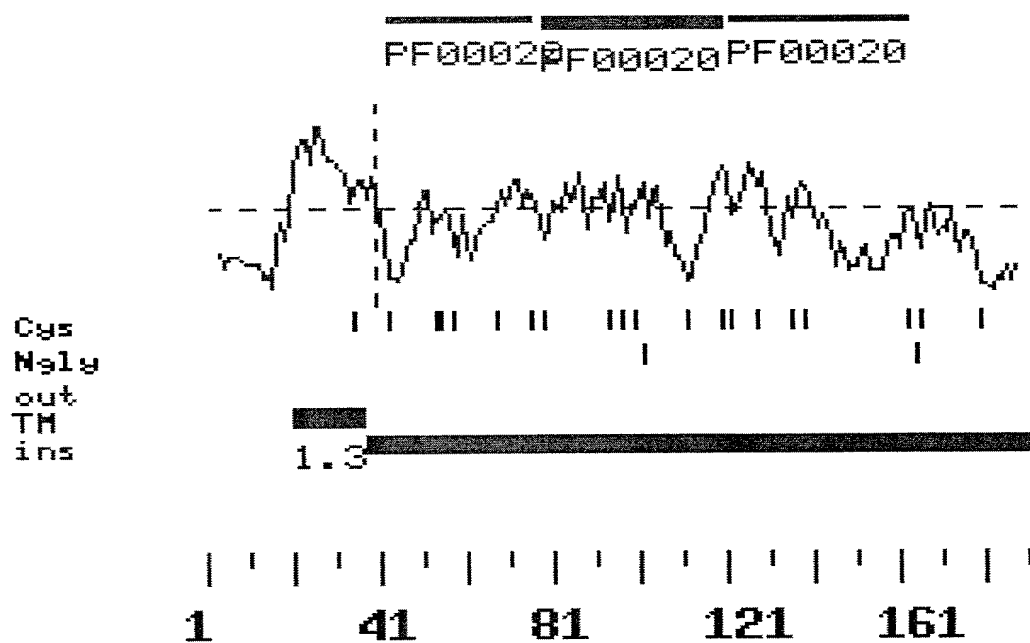


Figure 2

Input file T198sHVEM2; Output File T198sHVEM2.pat
Sequence length 1596

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S T P R T D V L R L V L Y L T F L G A P	33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC	205
C Y A P A L P S C K E D E Y P V G S E C	53
TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC	265
C P K C S P G Y R V K E A C G E L T G T	73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA	325
V C E P C P P G T Y I A H L N G L S K C	93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT	385
L Q C Q M C D P A M G L R A S R N C S R	113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG	445
P E N A V C G C S P G H F C I V Q D G D	133
ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC	505
H C A A C R A Y A T S S P G Q R V Q K G	153
CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA	565
G T E S Q D T L C Q N C P P G T F S P N	173
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT	625
G T L E E C Q H Q T N W P N H M C E K K	193
GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAT TGG CCT AAT CAT ATG TGT GAA AAG AAG	685
K A K G *	198
AAA GCC AAG GGG TGA	700
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CGTGCCATTCCCATGGGCCAGTGAGGGCTTGGGGCTCTGTTCTGTGTGGCTTGAGCTCCCCAGAGTCCTGAGGAGGA	1253
GCGCCAGTTGCCCTTCGCTCACAGACCACACACCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGT	1332
CTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTG	1411
CAGTGTGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGT	1490
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Figure 3

Figure 4

Input file sHVEM3; Output File sHVEM3.pat
Sequence length 2313

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GTCGACCCACGCGTCCGGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCTCGAGCTGCCGGTCTGAGCCT 79

      M   E   P   P   G   D   W   G   P   P   P   W   R   S   T   P   R   T      18
GAGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC      138

      D   V   S   R   L   V   L   Y   L   T   F   L   G   A   P   C   Y   A   P   A      38
GAC GTC TCG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT      198

      L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C   P   K   C   S      58
CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT      258

      P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   V   C   E   P   C      78
CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC      318

      P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   L   Q   C   Q   M      98
CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG      378

      C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   T   E   N   A   V      118
TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG      438

      C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   H   C   A   A   C      138
TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC      498

      R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   G   T   E   S   Q      158
CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG      558

      D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   T   L   E   E      178
GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA      618

      C   Q   H   Q   T   K   K   A   *
TGT CAG CAC CAG ACC AAA AAG GCT TGA      187
                                           645

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GCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAATGTGAGGGCCATGGGAGGGCC 882
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GGGCCCCTAACCTGACCTGAGACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCCAGCGAGCCTGGGATGGAGCAGGG 1040
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CAGTTGCCCTCTGCTCACAGACCACACACCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGTC 2146
GCGTCTGACTCTTGTGGCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGT 2225
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GGCGGCCG 2313

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Figure 5

407280-6347650

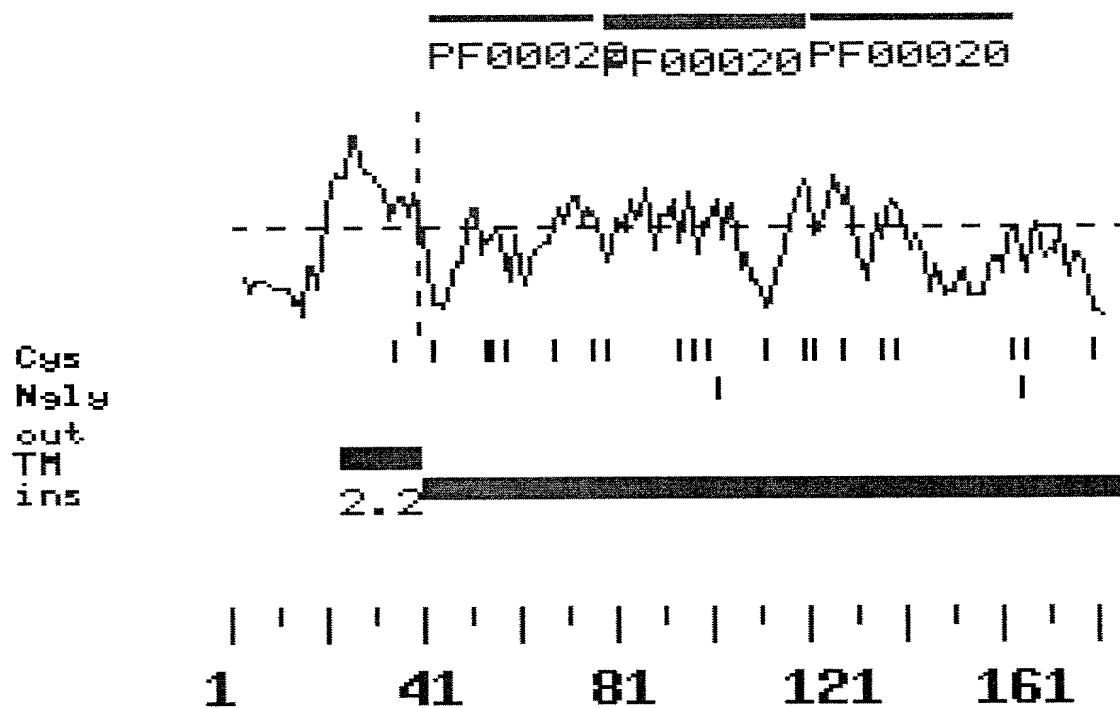


Figure 6

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AGCTGCCGGTCTGAGCCTGAGGC	144
T P R T D V L R L V L Y L T F L G A P C	34
ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC	204
Y A P A L P S C K E D E Y P V G S E C C	54
TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC	264
P K C S P G Y R V K E A C G E L T G T V	74
CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG	324
C E P C P P G T Y I A H L N G L S K C L	94
TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG	384
Q C Q M C D P A M G L R A S R N C S R T	114
CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA	444
E N A V C G C S P G H F C I V Q D G D H	134
GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC	504
C A A C R A Y A T S S P G Q R V Q K G G	154
TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC	564
E S Q D T L C Q N C P P G T F S P N G	174
ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG	624
L E E C Q H Q T K C S W L V T K A G A	194
ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC AGC TGG CTG GTG ACG AAG GCC GGA GCT	684
G T S S S H W V W W F L S G S L V I V I	214
GGG ACC AGC AGC TCC CAC TGG GTA TGG TGG TTT CTC TCA GGG AGC CTC GTC ATC GTC ATT	744
V C S T V G L I I C V K R R K P R G D V	234
GTT TGC TCC ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT GTA	804
V K V I V S V Q V L I L L P L S L P P P	254
GTC AAG GTG ATC GTC TCC GTC CAG GTA TTG ATC CTC CTC CCC CTC TCC CTC CCC CCT CCA	864
P S H L P S P R W G W C F W C T W W G L	274
CCT TCC CAC CTC CCC TCT CCC CGC TGG GGC TGG TGT TTC TGG TGT ACA TGG TGG GGG CTC	924
P V L *	278
CCA GTT CTC TGA	936
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Figure 7

PF00020 PF00020 PF00020

Cys
Ngly
out
TM
ins

2.5

7.2

1.9

1

41

81

121

161

201

241

Figure 8

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mHVEM_pub._n.a.	-----		
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shVEM_2_n.a.	-----		
shVEM_3_n.a.	AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC		
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mHVEM_pub._n.a.	-----G-----		
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shVEM_3_n.a.	TGCACCTGCCTCTCCCACGTCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
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shVEM_3_n.a.	AGCTCCCCTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGTCTCCACAGTTGGCCTAATCATATG		
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shVEM_3_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
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shVEM_3_n.a.	-----		
mHVEM_2_n.a.	TG--AGGGTCTGAG-TCTTTCAAGTACAGCCACGGTAGCTCAGGAAAAGAACCCACCCCTCAAAGTGAAGCAGTAAAA		
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shVEM_2_n.a.	TGA-----TGATGTC--AAGG----TGATC-----G-TCTCCA-----TC-CAGCGGAAAAGACA		
shVEM_3_n.a.	-----CAGCGGAAAAGACA		
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mHVEM_pub._n.a.	-----CAGCGGAAAAGACA		
	2161		2240
shVEM_1_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_2_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_3_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
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Figure 9C

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shVEM_1_n.a.	2321	2400
shVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_3_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
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shVEM_1_n.a.	2401	2480
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shVEM_1_n.a.	2481	2560
shVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCA	
shVEM_3_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCA	
mHVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCA	
mHVEM__pub.__n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCA	
shVEM_1_n.a.	2561	2640
shVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_3_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM__pub.__n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_1_n.a.	2641	2720
shVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTTTAGTGGATACACATCGG	
shVEM_3_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTTTAGTGGATACACATCGG	
mHVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTTTAGTGGATACACATCGG	
mHVEM__pub.__n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTTTAGTGGATACACATCGG	
shVEM_1_n.a.	2721	2800
shVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG	
shVEM_3_n.a.	AAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG	
mHVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG	
mHVEM__pub.__n.a.	AAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGCTGTG	
shVEM_1_n.a.	2801	2880
shVEM_2_n.a.	GGAGGATGTAAATATCTTGTCTCCTCAA----	
shVEM_3_n.a.	GGAGGATGTAAATATCTTGTCTCCTCAA----	
mHVEM_2_n.a.	GGAGGATGTAAATATCTTGTCTCCTCAA----	
mHVEM__pub.__n.a.	GGAGGATGTAAATATCTTGTCTCCTCAA----	
shVEM_1_n.a.	2881	2904
shVEM_2_n.a.	-----	
shVEM_3_n.a.	-----GGGCGGCCGC	
mHVEM_2_n.a.	AAAAAAAAAAAAAGGGCGGCCGC	
mHVEM__pub.__n.a.	-----	

Figure 9D

	1	80
shVEM_1_a.a.	MEPPGDWGPPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_2_a.a.	MEPPGDWGPPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_3_a.a.	MEPPGDWGPPPWRSTPRTDVSRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM_2_a.a.	MEPPGDWGPPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM__pub.__a.a.	MEPPGDWGPPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
	81	160
shVEM_1_a.a.	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_2_a.a.	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_3_a.a.	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM_2_a.a.	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM__pub.__a.a.	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
	161	240
shVEM_1_a.a.	LCQNCPPGTFSPNGTLEECQHQTNRawkSQTDL-----	
shVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTnWPNHMcEKKKAG-----	
shVEM_3_a.a.	LCQNCPPGTFSPNGTLEECQHQTkK-----	
mHVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTcSWLVTKAGAGTSSSHWVWwFLSGSLVIVIVcSTVGLIICVKKRKPRGDVVKVIVS	
mHVEM__pub.__a.a.	LCQNCPPGTFSPNGTLEECQHQTcSWLVTKAGAGTSSSHWVWwFLSGSLVIVIVcSTVGLIICVKKRKPRGDVVKVIVS	
	241	283
shVEM_1_a.a.	-----	
shVEM_2_a.a.	-----	
shVEM_3_a.a.	-----	
mHVEM_2_a.a.	VQVLILLPLSLPPPPSHLPSRWGWCfWCTWWGLPVL-----	
mHVEM__pub.__a.a.	VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPsFTGRSPNH	

Figure 10